

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) **APPLICANT:**

(A) NAME: Vlaamse Instelling voor Technologisch Onderzoek

(B) STREET: Boeretang 200

(C) CITY: Mol

(E) COUNTRY: Belgium

(F) POSTAL CODE (ZIP): 2400

(G) TELEPHONE: + 32 14 33 51 12

(H) TELEFAX: +32/ 14 32 03 72

(A) NAME: The University of Birmingham

(B) STREET: Edgbaston

(C) CITY: Birmingham

(E) COUNTRY: United Kingdom

(F) POSTAL CODE (ZIP): B15 2TT

(A) NAME: Lund University

(B) STREET: P.O. BOX 124

(C) CITY: Lund

(E) COUNTRY: Sweden

(F) POSTAL CODE (ZIP): 221 00

(ii) TITLE OF INVENTION: Metal ion-specific capacity affinity sensor

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER/READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) **SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) **HYPOTHETICAL: NO**

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Synechococcus* sp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly
 210 215 220
 Arg Gly Ile Pro Met Thr Ser Thr Thr Leu Val Lys Cys Ala Cys Glu
 225 230 235 240
 Pro Cys Leu Cys Asn Val Asp Pro Ser Lys Ala Ile Asp Arg Asn Gly
 245 250 255

Sub
 a/
 Contd.
 005007E 10500

22

Leu Tyr Tyr Cys Ser Glu Ala Cys Ala Asp Gly His Thr Gly Gly Ser
 260 265 270

Lys Gly Cys Gly His Thr Gly Cys Asn Cys Ser Glu Phe Ile Val Thr
 275 280 285

Asp

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Glu Asn Asn Leu Glu Asn Leu Thr Ile Gly Val Phe Ala Lys Ala
 1 5 10 15

Ala Gly Val Asn Val Glu Thr Ile Arg Phe Tyr Gln Arg Lys Gly Leu
 20 25 30

Leu Leu Glu Pro Asp Lys Pro Tyr Gly Ser Ile Arg Arg Tyr Gly Glu
 35 40 45

Ala Asp Val Thr Arg Val Arg Phe Val Lys Ser Ala Gln Arg Leu Gly
 50 55 60

Phe Ser Leu Asp Glu Ile Ala Glu Leu Leu Arg Leu Glu Asp Gly Thr
 65 70 75 80

His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val
 85 90 95

Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Ala Val Leu Ser Glu
 100 105 110

Sub
contd.
2205050

Leu Val Cys Ala Cys His Ala Arg Arg Gly Asn Val Ser Cys Pro Leu
115 120 125

Ile Ala Ser Leu Gln Gly Gly Ala Ser Leu Ala Gly Ser Ala Met Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) **HYPOTHETICAL: NO**

(iv) ANTI-SENSE: NO

(v) **FRAGMENT TYPE:** internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes eutrophus*
(B) STRAIN: CH34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Asn Ile Gln Ile Gly Glu Leu Ala Lys Arg Thr Ala Cys Pro Val
1 5 10 15

Val Thr Ile Arg Phe Tyr Glu Gln Glu Gly Leu Leu Pro Pro Pro Gly
20 25 30

Arg Ser Arg Gly Asn Phe Arg Leu Tyr Gly Glu Glu His Val Glu Arg
35 40 45

Leu Gln Phe Ile Arg His Cys Arg Ser Leu Asp Met Pro Leu Ser Asp
50 55 60

Val Arg Thr Leu Leu Ser Tyr Arg Lys Arg Pro Asp Gln Asp Cys Gly
65 70 75 80

Glu Val Asn Met Leu Leu Asp Glu His Ile Arg Gln Val Glu Ser Arg
85 90 95

Ile Gly Ala Leu Leu Glu Leu Lys His His Leu Val Glu Leu Arg Glu
100 105 110

Sub
a/
Contd.

Asp
145

Gly Tyr Pro Ser Ser Val Lys Gln
65 70